



9
0530
0620

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101084,507A
Source: OIPE
Date Processed by STIC: 7/2/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10084,507A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply OIPE
Corrected Diskette Needed

RAW SEQUENCE LISTING

DATE: 07/02/2002

See also p.12

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

W--> 1 ^{delete} 15
 4 <110> APPLICANT: MUNROE, Donald G.
 5 KAMBOJ, Rajender
 6 PETERS, Diana
 7 KOOSHESH, Fatemeh
 8 VYAS, Tejal B.
 9 GUPTA, Ashwani K.
 11 <120> TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN
 12 INFLAMMATORY RESPONSE
 14 <130> FILE REFERENCE: 8074-8021
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/084,507A
 C--> 17 <141> CURRENT FILING DATE: 2002-06-14
 19 <150> PRIOR APPLICATION NUMBER: 60/109,885
 20 <151> PRIOR FILING DATE: 1998-11-25
 22 <150> PRIOR APPLICATION NUMBER: 60/080,610
 23 <151> PRIOR FILING DATE: 1998-04-03
 25 <150> PRIOR APPLICATION NUMBER: 60/070,185
 26 <151> PRIOR FILING DATE: 1997-12-30
 28 <160> NUMBER OF SEQ ID NOS: 25
 30 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 35
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Rattus sp.
 37 <400> SEQUENCE: 1
 E--> 38 gagaaggttc aggaacacta caattacacc aagga
 39 ³⁵
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 25
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 47 <220> FEATURE:
 48 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 49 primer
 51 <400> SEQUENCE: 2
 E--> 52 attataccaa ggagacgctg gaaac
 53 ²⁵
 56 <210> SEQ ID NO: 3
 57 <211> LENGTH: 25

See error summary sheet item 1

global error: nucleic numbers
must be placed at the end of
the line, on the right margin

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

58 <212> TYPE: DNA
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 63 primer
 65 <400> SEQUENCE: 3

E--> 66 agagagcaag gtattggcta cgaag

67 25

70 <210> SEQ ID NO: 4

71 <211> LENGTH: 22

72 <212> TYPE: DNA

73 <213> ORGANISM: Artificial Sequence

75 <220> FEATURE:

76 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

77 primer

79 <400> SEQUENCE: 4

E--> 80 tcctctcctc gtcacatttc cc

81 22

84 <210> SEQ ID NO: 5

85 <211> LENGTH: 26

86 <212> TYPE: DNA

87 <213> ORGANISM: Artificial Sequence

89 <220> FEATURE:

90 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

91 primer

93 <400> SEQUENCE: 5

E--> 94 gcattcacaa gaaattactc tgaggc

95 26

98 <210> SEQ ID NO: 6

99 <211> LENGTH: 26

100 <212> TYPE: DNA

101 <213> ORGANISM: Artificial Sequence

103 <220> FEATURE:

104 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

105 primer

107 <400> SEQUENCE: 6

E--> 108 gagccccacc atgggcagct tgtact

109 26

112 <210> SEQ ID NO: 7

113 <211> LENGTH: 26

114 <212> TYPE: DNA

115 <213> ORGANISM: Artificial Sequence

117 <220> FEATURE:

118 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

119 primer

121 <400> SEQUENCE: 7

E--> 122 gcattcacaa gaaattactc tgaggc

123 26

126 <210> SEQ ID NO: 8

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

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129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
133     primer
135 <400> SEQUENCE: 8
E--> 136 tttaaaaagc ttcccacccat gggcagcttg tact
137 34
140 <210> SEQ ID NO: 9
141 <211> LENGTH: 37
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
147     primer
149 <400> SEQUENCE: 9
E--> 150 tatatatcta gacattcaca agaaattact ctgaggc
151 37
154 <210> SEQ ID NO: 10
155 <211> LENGTH: 32
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
161     primer
163 <400> SEQUENCE: 10
E--> 164 tatatatcta gaggaaatgt gacgaggaga gg
165 32
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 33
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
175     primer
177 <400> SEQUENCE: 11
E--> 178 tttaaaggta ccgccacccat gggcagcttg tac
179 33
182 <210> SEQ ID NO: 12
183 <211> LENGTH: 33
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
189     primer
191 <400> SEQUENCE: 12
E--> 192 tatatatcta gagaccaccg tgttgccctc cag
193 33

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RAW SEQUENCE LISTING

DATE: 07/02/2002

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TIME: 10:05:44

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Output Set: N:\CRF3\07022002\J084507A.raw

196 <210> SEQ ID NO: 13
 197 <211> LENGTH: 445
 198 <212> TYPE: DNA
 199 <213> ORGANISM: Homo sapiens
 201 <400> SEQUENCE: 13

E--> 202 aaagcccat ggcccagca ggcctctgag cccaccatg ggcagcttgt actcggagta
 203 60

E--> 204 cctgaacccc aacaagggtcc aggaacacta taattatacc aaggagacgc tggaaacgca
 205 120

E--> 206 ggagacgacc tcccgccagg tggcctcggc attcatcgtc atcctctgtt gcgccattgt
 207 180

E--> 208 ggtggaaaac cttctggtgc tcattgcggt ggcccgaac agcaagttcc actcggcaat
 209 240

E--> 210 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc
 211 300

E--> 212 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg
 213 360

E--> 214 ggacgggtctg ccttcatcac gctctcggcc tctgtcttca gcctcctggc catcgccatt
 215 420

E--> 216 ggcgcacg tggccattgc aaagg
 217 445

220 <210> SEQ ID NO: 14
 221 <211> LENGTH: 364
 222 <212> TYPE: DNA
 223 <213> ORGANISM: Homo sapiens
 225 <400> SEQUENCE: 14

E--> 226 aaagcccat ggcccagca ggcctctgag cccaccatg ggcagcttgt actcggagta
 227 60

E--> 228 cctgaacccc aacaagggtcc aggaacacta taattatacc aaggagacgc tggaaacgca
 229 120

E--> 230 ggagacgacc tcccgccagg tggcctcggc cttcatcgtc atcctctgtt gcgccattgt
 231 180

E--> 232 ggtggaaaac cttctggtgc tcattgcggt ggcccgaac agcaagttcc actcggcaat
 233 240

E--> 234 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc
 235 300

E--> 236 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg
 237 360

E--> 238 ggac
 239 364

242 <210> SEQ ID NO: 15
 243 <211> LENGTH: 369
 244 <212> TYPE: DNA
 245 <213> ORGANISM: Homo sapiens
 247 <400> SEQUENCE: 15

E--> 248 agttctgaaa gcccattggc cccagcaggc ctctgagccc caccatgggc agcttgtagt
 249 60

E--> 250 cggagtacct gaacccaac aagggtccagg aacactataa ttataccaag gagacgctgg
 251 120

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E--> 252 aaacgcagga gacgacctcc cgccagggtgg gctcggcctt catcgctcatc ctctgttgcg
      253 180
E--> 254 ccattgtggt ggaaaacctt ctggtgctca ttgcggtggc ccgaaacagc aagttccact
      255 240
E--> 256 cggcaatgta cctgtttctg ggcaacctgg ccgcctccga tctactggca ggcgtggcct
      257 300
E--> 258 cgtagccaat accttgcctt ctggctctgt cacgctgagg ctgacgcctg tgcagtgggt
      259 360
E--> 260 tgccccggga
      261 369
      264 <210> SEQ ID NO: 16
      265 <211> LENGTH: 1170
      266 <212> TYPE: DNA
      267 <213> ORGANISM: Homo sapiens
      269 <220> FEATURE:
      270 <221> NAME/KEY: CDS
      271 <222> LOCATION: (38)..(1096)
      273 <400> SEQUENCE: 16
E--> 274 aaagccccat ggccccagca ggccctctgag ccccacc atg ggc agc ttg tac tcg
      275 55
      276
      277
      Met Gly Ser Leu Tyr Ser
      1 5
E--> 279 gag tac ctg aac ccc aac aag gtc cag gaa cac tat aat tat acc aag
      280 103
      281 Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu His Tyr Asn Tyr Thr Lys
      282 10 15 20
E--> 284 gag acg ctg gaa acg cag gag acg acc tcc cgc cag gtg gcc tcg gcc
      285 151
      286 Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser Arg Gln Val Ala Ser Ala
      287 25 30 35
E--> 289 ttc atc gtc atc ctc tgt tgc gcc att gtg gtg gaa aac ctt ctg gtg
      290 199
      291 Phe Ile Val Ile Leu Cys Cys Ala Ile Val Val Glu Asn Leu Leu Val
      292 40 45 50
E--> 294 ctc att gcg gtg gcc cga aac agc aag ttc cac tcg gca atg tac ctg
      295 247
      296 Leu Ile Ala Val Ala Arg Asn Ser Lys Phe His Ser Ala Met Tyr Leu
      297 55 60 65 70
E--> 299 ttt ctg ggc aac ctg gcc gcc tcc gat cta ctg gca ggc gtg gcc ttc
      300 295
      301 Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu Leu Ala Gly Val Ala Phe
      302 75 80 85
E--> 304 gta gcc aat acc ttg ctc tct ggc tct gtc acg ctg agg ctg acg cct
      305 343
      306 Val Ala Asn Thr Leu Leu Ser Gly Ser Val Thr Leu Arg Leu Thr Pro
      307 90 95 100
E--> 309 gtg cag tgg ttt gcc cgg gag ggc tct gcc ttc atc acg ctc tcg gcc
      310 391
      311 Val Gln Trp Phe Ala Arg Glu Gly Ser Ala Phe Ile Thr Leu Ser Ala

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Input Set : A:\100879_1.asc

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      312      105      110      115
E--> 314 tct gtc ttc agc ctc ctg gcc atc gcc att gag cgc cac gtg gcc att
      315 439
      316 Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg His Val Ala Ile
      317      120      125      130
E--> 319 gcc aag gtc aag ctg tat ggc agc gac aag agc tgc cgc atg ctt ctg
      320 487
      321 Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys Ser Cys Arg Met Leu Leu
      322 135      140      145      150
E--> 324 ctc atc ggg gcc tcg tgg ctc atc tcg ctg gtc ctc ggt ggc ctg ccc
      325 535
      326 Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu Val Leu Gly Gly Leu Pro
      327      155      160      165
E--> 329 atc ctt ggc tgg aac tgc ctg ggc cac ctc gag gcc tgc tcc act gtc
      330 583
      331 Ile Leu Gly Trp Asn Cys Leu Gly His Leu Glu Ala Cys Ser Thr Val
      332      170      175      180
E--> 334 ctg cct ctc tac gcc aag cat tat gtg ctg tgc gtg gtg acc atc ttc
      335 631
      336 Leu Pro Leu Tyr Ala Lys His Tyr Val Leu Cys Val Val Thr Ile Phe
      337      185      190      195
E--> 339 tcc atc atc ctg ttg gcc atc gtg gcc ctg tac gtg cgc atc tac tgc
      340 679
      341 Ser Ile Ile Leu Leu Ala Ile Val Ala Leu Tyr Val Arg Ile Tyr Cys
      342      200      205      210
E--> 344 gtg gtc cgc tca agc cac gct gac atg gcc gcc ccg cag acg cta gcc
      345 727
      346 Val Val Arg Ser Ser His Ala Asp Met Ala Ala Pro Gln Thr Leu Ala
      347 215      220      225      230
E--> 349 ctg ctc aag acg gtc acc atc gtg cta ggc gtc ttt atc gtc tgc tgg
      350 775
      351 Leu Leu Lys Thr Val Thr Ile Val Leu Gly Val Phe Ile Val Cys Trp
      352      235      240      245
E--> 354 ctg ccc gcc ttc agc atc ctc ctt ctg gac tat gcc tgt ccc gtc cac
      355 823
      356 Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp Tyr Ala Cys Pro Val His
      357      250      255      260
E--> 359 tcc tgc ccg atc ctc tac aaa gcc cac tac ytt ttc gcc gtc tcc acc
      360 871
W--> 361 Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr Xaa Phe Ala Val Ser Thr
      362      265      270      275
E--> 364 ctg aat tcc ctg ctc aac ccc gtc atc tac acg tgg cgc agc cgg gac
      365 919
      366 Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr Thr Trp Arg Ser Arg Asp
      367      280      285      290
E--> 369 ctg cgg cgg gag gtg ctt cgg ccg ctg cag tgc tgg cgg ccg ggg gtg
      370 967
      371 Leu Arg Arg Glu Val Leu Arg Pro Leu Gln Cys Trp Arg Pro Gly Val
      372 295      300      305      310

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Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

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E--> 374 ggg gtg caa gga cgg agg cgg ggc ggg acc ccg ggc cac cac ctc ctg
375 1015
376 Gly Val Gln Gly Arg Arg Arg Gly Gly Thr Pro Gly His His Leu Leu
377          315          320          325
E--> 379 cca ctc cgc agc tcc agc tcc ctg gag agg ggc atg cac atg ccc acg
380 1063
381 Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg Gly Met His Met Pro Thr
382          330          335          340
E--> 384 tca ccc acg ttt ctg gag ggc aac acg gtg gtc tgaggggtggg ggtgggaccaa
385 1116
386 Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val
387          345          350
E--> 389 caaccaggcc agggcatagg ggttcatgga aaggccactg ggtgacccca aata
390 1170
393 <210> SEQ ID NO: 17
394 <211> LENGTH: 353
395 <212> TYPE: PRT
396 <213> ORGANISM: Homo sapiens
398 <400> SEQUENCE: 17
399 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
400 1          5          10          15
402 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
403          20          25          30
405 Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
406          35          40          45
408 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
409          50          55          60
411 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
412 65          70          75          80
414 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
415          85          90          95
417 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
418          100          105          110
420 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
421          115          120          125
423 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
424          130          135          140
426 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
427 145          150          155          160
429 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
430          165          170          175
432 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
433          180          185          190
435 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
436          195          200          205
438 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
439 210          215          220
441 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
442 225          230          235          240

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Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

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444 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
445                245                250                255
447 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
448                260                265                270
E--> 450 Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
451                275                280                285
453 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
454                290                295                300
456 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr
457 305                310                315                320
459 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
460                325                330                335
462 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
463                340                345                350
465 Val
470 <210> SEQ ID NO: 18
471 <211> LENGTH: 1170
472 <212> TYPE: DNA
473 <213> ORGANISM: Homo sapiens
475 <400> SEQUENCE: 18
E--> 476 tttcggggta ccggggtcgt ccggagactc ggggtggtac ccgtcgaaca tgagcctcat
477 60
E--> 478 ggacttgggg ttgttccagg tccttgtgat attaatatgg ttcctctgcg acctttgcgt
479 120
E--> 480 cctctgctgg agggcggtcc accggagccg gaagtagcag taggagacaa cgcggtaaca
481 180
E--> 482 ccaccttttg gaagaccacg agtaacgcca ccgggctttg tcgttcaagg tgagccgtta
483 240
E--> 484 catggacaaa gaccctgttg accggcgagg gctagatgac cgcccgacc ggaagcatcg
485 300
E--> 486 gttatggaac gagagaccga gacagtgcga ctccgactgc ggacacgtca ccaaacgggc
487 360
E--> 488 cctcccgaga cggaagtagt gcgagagccg gagacagaag tcggaggacc ggtagcggta
489 420
E--> 490 actcgcggtg caccggtaac ggttccagtt cgacataccg tcgctgttct cgacggcgta
491 480
E--> 492 cgaagacgag tagccccgga gcaccgagta gagcgaccag gagccaccgg acgggtagga
493 540
E--> 494 accgaccttg acggaccggg tggagctccg gacgaggtga caggacggag agatgcggtt
495 600
E--> 496 cgtaatacac gacacgcacc actggtagaa gaggtagtag gacaaccggt agcaccggga
497 660
E--> 498 catgcacgcg tagatgacgc accaggcgag ttcggtgcga ctgtaccggc ggggcgtctg
499 720
E--> 500 cgatcggggac gagttctgcc agtggttagca cgatccgcag aaatagcaga cgaccgacgg
501 780
E--> 502 gcggaagtcg taggaggaag acctgatacg gacagggcag gtgaggacgg gctaggagat
503 840
E--> 504 gtttcgggtg atgraaaagc ggcagaggtg ggacttaagg gacgagttgg ggcagtagat

```

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

```

505 900
E--> 506 gtgcaccgcg tcggccctgg acgccgccct ccacgaagcc ggcgacgtna cgaccgccgg
507 960
E--> 508 cccccacccc cacgttcctg cctccgcccc gccctggggc ccggtgggtg aggacgggtga
509 1020
E--> 510 ggcgtcgagg tcgagggacc tctccccgta cgtgtacggg tgcagtgggt gaaaagacct
511 1080
E--> 512 cccgttgtgc caccagactc ccacccccac ctgggtgttg gtccgggtccc gtatccccaa
513 1140
E--> 514 gtacctttcc ggtgaccac tggggtttat
515 1170
518 <210> SEQ ID NO: 19
519 <211> LENGTH: 1062
520 <212> TYPE: DNA
521 <213> ORGANISM: Homo sapiens
523 <400> SEQUENCE: 19
E--> 524 atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat
525 60
E--> 526 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcac
527 120
E--> 528 gtcacctctt gttgcgccat tgtggtggaa aaccttctgg tgetcattgc ggtggcccg
529 180
E--> 530 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta
531 240
E--> 532 ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggctg
533 300
E--> 534 acgcctgtgc agtggtttgc ccgggagggc tctgccttca tcacgctctc ggcctctgtc
535 360
E--> 536 ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggc caagctgtat
537 420
E--> 538 ggcagcgaca agagctgccg catgcttctg ctcacgggg cctcgtgggt catctcgtg
539 480
E--> 540 gtccctcggtg gcctgcccac ccttggctgg aactgcctgg gccacctcga ggcctgctcc
541 540
E--> 542 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtgacctt cttctccatc
543 600
E--> 544 atcctgttgg ccgtcgtggc cctgtacgtg cgcattctact gcgtgggtccg ctcaagccac
545 660
E--> 546 gctgacatgg ccgccccgca gacgctagcc ctgctcaaga cggtcacat cgtgctaggc
547 720
E--> 548 gtctttatcg tctgctgggt gcccgcttc agcatcctcc ttctggacta tgccctgtcc
549 780
E--> 550 gtccactcct gcccgatcct ctacaaagcc cactacctt tcgccgtctc caccctgaat
551 840
E--> 552 tccctgtcga accccgtcat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt
553 900
E--> 554 cggccgctgc agtgetggcg gccgggggtg ggggtgcaag gacggaggcg gggcgggacc
555 960
E--> 556 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg

```

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

```

557 1020
E--> 558 cccacgtcac ccacgtttct ggagggcaac acggtggtct ga
559 1062
562 <210> SEQ ID NO: 20
563 <211> LENGTH: 1062
564 <212> TYPE: DNA
565 <213> ORGANISM: Homo sapiens
567 <400> SEQUENCE: 20
E--> 568 taccctgcga acatgagcct catggacttg gggttgttcc aggtccttgt gatattaata
569 60
E--> 570 tggttcctct gcgacctttg cgtcctctgc tggagggcgg tccaccggag ccggaagtag
571 120
E--> 572 cagtaggaga caacgcggta acaccacctt ttggaagacc acgagtaacg ccaccgggct
573 180
E--> 574 ttgtcgttca aggtgagccg ttacatggac aaagaccctt tggaccggcg gaggctagat
575 240
E--> 576 gaccgtccgc accggaagca tcggttatgg aacgagagac cgagacagtg cgactccgac
577 300
E--> 578 tgcggacacg tcaccaaacg ggccctcccc agacggaagt agtgcgagag ccggagacag
579 360
E--> 580 aagtcggagg accggtagcg gtaactcgcg gtgcaccggt aacggttcca gttcgacata
581 420
E--> 582 ccgtcgctgt tctcgacggc gtacgaagac gagtagcccc ggagcaccga gtagagcgac
583 480
E--> 584 caggagccac cggacgggta ggaaccgacc ttgacggacc cggtggagct ccggacgagg
585 540
E--> 586 tgacaggacg gagagatgcg gttcgtaata cacgacacgc accactggta gaagaggtag
587 600
E--> 588 taggacaacc ggcagcaccg ggacatgcac gcgtagatga cgcaccaggc gagttcggtg
589 660
E--> 590 cgactgtacc ggcggggcgt ctgcgatcgg gacgagttct gccagtggta gcacgatccg
591 720
E--> 592 cagaaatagc agacgaccga cgggcggaag tcgtaggagg aagacctgat acggacaggg
593 780
E--> 594 caggtaggga cgggctagga gatgtttcgg gtgatggaaa agcggcagag gtgggactta
595 840
E--> 596 agggacgagt tggggcagta gatgtgcacc gcgtcggccc tggacgccgc cctccacgaa
597 900
E--> 598 gccggcgacg tcacgaccgc cggccccac cccacgttc ctgcctccgc cccgccctgg
599 960
E--> 600 ggcccgggtg tggaggacgg tgaggcgtcg aggtcgaggg acctctcccc gtacgtgtac
601 1020
E--> 602 ggggtgcagt ggtgcaaaga cctcccgttg tgccaccaga ct
603 1062
831 <210> SEQ ID NO: 24
832 <211> LENGTH: 1056
833 <212> TYPE: DNA
834 <213> ORGANISM: Homo sapiens
836 <400> SEQUENCE: 24

```

RAW SEQUENCE LISTING

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:44

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

E--> 837 atggtcatca tgggccagtg ctactacaac gagaccatcg gcttcttcta taacaacagt
838 60
E--> 839 ggcaaagagc tcagctccca ctggcgggccc aaggatgtgg tcgtggtggc actggggctg
840 120
E--> 841 accgtcagcg tgctggtgct gctgaccaat ctgctgggtca tagcagccat cgcctccaac
842 180
E--> 843 cgccgcttcc accagcccat ctactacctg ctcggcaatc tggccgcggc tgacctcttc
844 240
E--> 845 gcgggctggg cctacctctt cctcatgttc cacactggtc cccgcacagc ccgactttca
846 300
E--> 847 cttgagggct ggttcctgcg gcagggttg ctggacacaa gcctcaactgc gtcgggtggc
848 360
E--> 849 acactgctgg ccacgcgcgt ggagcgggcac cgcagtgtga tggccgtgca gctgcacagc
850 420
E--> 851 cgcctgcccc gtggccgcgt ggtcatgctc attgtgggcg tgtgggtggc tgccctgggc
852 480
E--> 853 ctggggctgc tgcccgccca ctccctggcac tgccctctgt ccctggaccg ctgctcacgc
854 540
E--> 855 atggcacccc tgctcagccg ctccctatttg gccgtctggg ctctgtcgag cctgcttgct
856 600
E--> 857 ttccctgctca tgggtggtgt gtacacccgc attttcttct acgtgcggcg gcgagtgcag
858 660
E--> 859 cgcattggcag agcatgtcag ctgccacccc cgctaccgag agaccacgct cagcctggtc
860 720
E--> 861 aagactgttg tcatcatcct gggggcggtc gtggtctgct ggacaccagg ccagggtgta
862 780
E--> 863 ctgctcctgg atggttttagg ctgtgagtc tgcaatgtcc tggctgtaga aaagtacttc
864 840
E--> 865 ctactgctgg ccgaggccaa ctcaactggc aatgctgctg tgtactcttg ccgagatgct
866 900
E--> 867 gagatgcgcc gcaccttccg ccgccttctc tgetgcgcgt gcctccgcca gtccacccgc
868 960
E--> 869 gagtctgtcc actatacatc ctctgcccag ggagggtgcca gcactcgcat catgcttccc
870 1020
E--> 871 gagaacggcc acccactgat ggactccacc ctttag
872 1056

VARIABLE LOCATION SUMMARY

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:45

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:16; Xaa Pos. 273

Seq#:17; Xaa Pos. 273

Seq#:18; N Pos. 949

VERIFICATION SUMMARY

DATE: 07/02/2002

PATENT APPLICATION: US/10/084,507A

TIME: 10:05:45

Input Set : A:\100879_1.asc

Output Set: N:\CRF3\07022002\J084507A.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:1
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:2
L:66 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:3
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:4
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:6
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:7
L:136 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:8
L:150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:9
L:164 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:10
L:178 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:11
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:12
L:202 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
M:254 Repeated in SeqNo=13
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
M:254 Repeated in SeqNo=14
L:248 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
M:254 Repeated in SeqNo=15
L:274 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:16
M:254 Repeated in SeqNo=16
L:361 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:871
L:450 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:476 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
M:254 Repeated in SeqNo=18
M:340 Repeated in SeqNo=18
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:568 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
M:254 Repeated in SeqNo=20
L:837 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:24
M:254 Repeated in SeqNo=24
L:881 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:25
M:254 Repeated in SeqNo=25